



SEQUENCE LISTING

<110> Yeh, Chau-Ting

<120> NOVEL VIRAL SEQUENCES

<130> 14176-003001

<140> US 10/730,632

<141> 2003-12-08

<150> US 60/440,948

<151> 2003-01-17

<160> 9

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 364

<212> DNA

<213> Unknown

<220>

<221> CDS

<222> (1)...(364)

<223> Viral sequence NV-F

<400> 1

gac	tgt	tgg	tgg	cac	aaa	gcc	ccg	agc	aaa	gtt	ggc	aac	ccc	cgc	cgt	48
Asp	Cys	Trp	Trp	His	Lys	Ala	Pro	Ser	Lys	Val	Gly	Asn	Pro	Arg	Arg	
1				5				10						15		

cac	tca	gcc	ctg	caa	gaa	gcc	act	tgc	gtc	ctc	cac	aac	tcc	cca	aag	96
His	Ser	Ala	Leu	Gln	Glu	Ala	Thr	Cys	Val	Leu	His	Asn	Ser	Pro	Lys	
		20						25						30		

ttg	tta	ctg	gtg	tac	caa	tcg	gag	gca	gcc	gag	ggg	atg	tat	aaa	gaa	144
Leu	Leu	Leu	Val	Tyr	Gln	Ser	Glu	Ala	Ala	Glu	Gly	Met	Tyr	Lys	Glu	
		35					40					45				

ata	gca	aag	gaa	ttc	gcg	aaa	ggg	aaa	gga	aag	aag	gag	agg	aaa	cta	192
Ile	Ala	Lys	Glu	Phe	Ala	Lys	Gly	Lys	Gly	Lys	Lys	Glu	Arg	Lys	Leu	
	50					55					60					

aag	aag	aaa	aaa	atg	ctt	tcg	ggt	att	acg	gaa	gaa	ggt	tct	cca	cag	240
Lys	Lys	Lys	Lys	Met	Leu	Ser	Gly	Ile	Thr	Glu	Glu	Gly	Ser	Pro	Gln	
	65				70				75						80	

cag	tcc	tct	tct	gct	ccg	ggc	ctg	gag	gga	gag	agc	gag	acc	aca	aag	288
Gln	Ser	Ser	Ser	Ala	Pro	Gly	Leu	Glu	Gly	Glu	Ser	Glu	Thr	Thr	Lys	
				85				90						95		

atg	atg	agc	aaa	aaa	ttc	caa	gac	atg	acg	aat	ccg	caa	aag	aag	aaa	336
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Met Met Ser Lys Lys Phe Gln Asp Met Thr Asn Pro Gln Lys Lys Lys
 100 105 110

aag aaa cgg acc agt ctg ctc ctt aac t
 Lys Lys Arg Thr Ser Leu Leu Leu Asn
 115 120

364

<210> 2
 <211> 121
 <212> PRT
 <213> Unknown

<220>
 <223> Viral sequence NV-F

<400> 2
 Asp Cys Trp Trp His Lys Ala Pro Ser Lys Val Gly Asn Pro Arg Arg
 1 5 10 15
 His Ser Ala Leu Gln Glu Ala Thr Cys Val Leu His Asn Ser Pro Lys
 20 25 30
 Leu Leu Leu Val Tyr Gln Ser Glu Ala Ala Glu Gly Met Tyr Lys Glu
 35 40 45
 Ile Ala Lys Glu Phe Ala Lys Gly Lys Gly Lys Lys Glu Arg Lys Leu
 50 55 60
 Lys Lys Lys Lys Met Leu Ser Gly Ile Thr Glu Glu Gly Ser Pro Gln
 65 70 75 80
 Gln Ser Ser Ser Ala Pro Gly Leu Glu Gly Glu Ser Glu Thr Thr Lys
 85 90 95
 Met Met Ser Lys Lys Phe Gln Asp Met Thr Asn Pro Gln Lys Lys Lys
 100 105 110
 Lys Lys Arg Thr Ser Leu Leu Leu Asn
 115 120

<210> 3
 <211> 20
 <212> DNA
 <213> Unknown

<220>
 <223> Primer

<400> 3
 tggttggtggc acaaagcccc

20

<210> 4
 <211> 20
 <212> DNA
 <213> Unknown

<220>
 <223> Primer

<400> 4
 ctttgtgggc tcgctctctc

20

<210> 5

<211> 20
 <212> DNA
 <213> Unknown

<220>
 <223> Primer

<400> 5
 gcaaagttgg caacccccgc 20

<210> 6
 <211> 20
 <212> DNA
 <213> Unknown

<220>
 <223> Primer

<400> 6
 ctccaggccc ggagcagaag 20

<210> 7
 <211> 10
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<221> misc_feature
 <222> 7-10
 <223> n = mixture of A, T, C, and G in equal ratios

<400> 7
 ccgcggnnnn 10

<210> 8
 <211> 10
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<221> misc_feature
 <222> 7-10
 <223> n = mixture of A, T, C, and G in equal ratios.

<400> 8
 gaattcnnnn 10

<210> 9
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Primer

<400> 9

gcttgctctg tctctttttt tttttttttt tttt

34